

## SEQUENCE LISTING

	<110		Wei, Guo, Zhang	Rong	gbing	3												
	<120	>	> Recombinant Super-Compound Interferon															
	<130	>	792-1	A-PC	r-US													
	<140 <141		10/6! 2003	•														
	<150 <151		PCT/CN02/00128 2002-02-28															
	<150 <151		CN 01104367.9 2001-02-28															
	<160	>	13															
	<170	>	Pate	ntIn	vers	sion	3.2											
•	<210 <211 <212 <213	.> :>	1 504 DNA huma:	n syı	nthes	sis											-	
	<220 <221 <222	. >	CDS (1).	. (504	<del>1</del> )													
	<400		1 gac	cta	cca	cac	200	cac	tcc	cta	aat	220	cat	aat	aat	ata		4.0
	Met 1	Cys	Asp	Leu	Pro 5	Gln	Thr	His	Ser	Leu 10	Gly	Asn	Arg	Arg	Ala 15	Leu		48
	atc Ile	ctg Leu	ctg Leu	gct Ala 20	cag Gln	atg Met	cgt Arg	cgt Arg	atc Ile 25	tcc Ser	ccg Pro	ttc Phe	tcc Ser	tgc Cys 30	ctg Leu	aaa Lys		96
	gac Asp	cgt Arg	cac His 35	gac Asp	ttc Phe	ggt Gly	ttc Phe	ccg Pro 40	cag Gln	gaa Glu	gaa Glu	ttc Phe	gac Asp 45	ggt Gly	aac Asn	cag Gln		144
	ttc Phe	cag Gln 50	aaa Lys	gct Ala	cag Gln	gct Ala	atc Ile 55	tcc Ser	gtt Val	ctg Leu	cac His	gaa Glu 60	atg Met	atc Ile	cag Gln	cag Gln		192
	acc Thr 65	ttc Phe	aac Asn	ctg Leu	ttc Phe	tcc Ser 70	acc Thr	aaa Lys	gac Asp	tcc Ser	tcc Ser 75	gct Ala	gct Ala	tgg Trp	gac Asp	gaa Glu 80		240
	tcc Ser	ctg Leu	ctg Leu	gaa Glu	aaa Lys 85	ttc Phe	tac Tyr	acc Thr	gaa Glu	ctg Leu 90	tac Tyr	cag Gln	cag Gln	ctg Leu	aac Asn 95	gac Asp		288

10	c gtt atc s Val Ile 0						
atg aac gtt ga Met Asn Val As 115							
acc ctg tac ct Thr Leu Tyr Le 130							
gtt cgt gct ga Val Arg Ala Gl 145							Ĺ
gaa cgt ctg cg Glu Arg Leu Ar							504
<210> 2 <211> 167 <212> PRT <213> human s	ynthesis						
<400> 2							
Met Cys Asp Le	u Pro Gln	Thr His	Ser Leu	Gly Asn	Arg Arg	Ala Leu	L
1	5		10	•		15	
		Arg Arg				15	
1 Ile Leu Leu Al	a Gln Met		Ile Ser 25	Pro Phe	Ser Cys 30	15 Leu Lys	
Ile Leu Leu Al 20 Asp Arg His As	a Gln Met o Phe Gly	Phe Pro 40	Ile Ser 25 Gln Glu	Pro Phe Glu Phe	Ser Cys 30 Asp Gly 45	Leu Lys	ı
Ile Leu Leu Al 20 Asp Arg His As 35 Phe Gln Lys Al	a Gln Met o Phe Gly a Gln Ala	Phe Pro 40 Ile Ser 55	Ile Ser 25 Gln Glu Val Leu	Pro Phe Glu Phe His Glu 60	Ser Cys 30 Asp Gly 45	Leu Lys Asn Gln Gln Gln	
Ile Leu Leu Al 20 Asp Arg His As 35 Phe Gln Lys Al 50 Thr Phe Asn Le	a Gln Met  Phe Gly  Gln Ala  Phe Ser  70	Phe Pro 40  Ile Ser 55  Thr Lys	Ile Ser 25 Gln Glu Val Leu Asp Ser	Pro Phe Glu Phe His Glu 60 Ser Ala 75	Ser Cys 30 Asp Gly 45 Met Ile	Leu Lys Asn Gln Gln Gln Asp Glu 80	

Met	Asn	Val 115	Asp	Ser	Ile	Leu	Ala 120	Val	Lys	Lys	Tyr	Phe 125	Gln	Arg	Ile	
Thr	Leu 130	Tyr	Leu	Thr	Glu	Lys 135	Lys	Tyr	Ser	Pro	Cys 140	Ala	Trp	Glu	Val	
Val 145	Arg	Ala	Glu	Ile	Met 150	Arg	Ser	Phe	Ser	Leu 155	Ser	Thr	Asn	Leu	Gln 160	
Glu	Arg	Leu	Arg	Arg 165	Lys	Glu										
<210 <211 <212 <213	L> : 2> 1	3 360 ONA numan	n syr	nthe	sis											
<220 <221 <222	L> (	CDS	. (360	0)												
	tgt								ctt Leu 10							48
att Ile	ctg Leu	ctg Leu	gca Ala 20	cag Gln	atg Met	cgt Arg	cgt Arg	att Ile 25	tcc Ser	ccg Pro	ttt Phe	agc Ser	tgc Cys 30	ctg Leu	aaa Lys	96
gac Asp	cgt Arg	cac His 35	gac Asp	ttc Phe	ggc	ttt Phe	ccg Pro 40	caa Gln	gaa Glu	gag Glu	ttc Phe	gat Asp 45	ggc Gly	aac Asn	caa Gln	144
ttc Phe	cag Gln 50	aaa Lys	gct Ala	cag Gln	gca Ala	atc Ile 55	tct Ser	gta Val	ctg Leu	cac His	gaa Glu 60	atg Met	atc Ile	caa Gln	cag Gln	192
acc Thr 65	ttc Phe	aac Asn	ctg Leu	ttt Phe	tcc Ser 70	act Thr	aaa Lys	gac Asp	agc Ser	tct Ser 75	gct Ala	gct Ala	tgg Trp	gac Asp	gaa Glu 80	240
agc Ser	ttg Leu	ctg Leu	gag Glu	aag Lys 85	ttc Phe	tac Tyr	act Thr	gaa Glu	ctg Leu 90	tat Tyr	cag Gln	cag Gln	ctg Leu	aac Asn 95	gac Asp	288
ctg Leu	gaa Glu	gca Ala	tgc Cys 100	gta Val	atc Ile	cag Gln	gaa Glu	gtt Val 105	ggt Gly	gta Val	gaa Glu	gag Glu	act Thr 110	ccg Pro	ctg Leu	336
		gtc Val														360

.

.

115 120

<210> 4
<211> 120
<212> PRT

<213> human synthesis

<400> 4

Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu  $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10 \hspace{1.5cm} 15$ 

Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
20 25 30

Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln 35 40 45

Phe Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln 50 55 60

Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu 65 70 75 80

Ser Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp 85 90 95

Leu Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu 100 105 110

Met Asn Val Asp Ser Ile Leu Ala 115 120

<210> 5

<211> 108 <212> DNA

<213> chemical synthesis

<220>

<221> CDS

<222> (1)..(108)

<400> 5

atg tgc gac ctg ccg cag acc cac tcc ctg ggt aac cgt cgt gct ctg Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu 1 5 10 15

48

```
atc ctg ctg gct cag atg cgt cgt atc tcc ccg ttc tcc tgc ctg aaa
                                                                       96
Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
            20
gac cgt cac gac
                                                                      108
Asp Arg His Asp
        35
<210>
       6
<211>
<212>
<213> chemical synthesis
<400> 6
Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu
                5
                                    10
Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
            20
                                25
                                                    30
Asp Arg His Asp
        35
<210> 7
<211> 107
<212> DNA
<213> chemical systhesis
<220>
<221> Unsure
<222>
      (1)..(107)
ctgaaagacc gtcacgactt cggtttcccg caggagaggt tcgacggtaa ccagttccag
aagctcaggc tatctccgtt ctgcacgaaa tgatccagca gaccttc
                                                                      107
<210> 8
<211> 103
<212> DNA
<213> chemical systhesis
<220>
<221> Unsure
<222> (1)..(103)
gctgctggta cagttcggtg tagaattttt ccagcaggga ttcgtcccaa gcagcggagg
                                                                       60
```

```
agtctttggt ggagaacagg ttgaaggtct gctggatcat ttc
                                                                    103
<210> 9
<211>
      103
<212> DNA
<213> chemical systhesis
<220>
<221> Unsure
<222> (1)..(103)
<400> 9
atccctgctg gaaaaattct acaccgaact gtaccagcag ctgaacgacc tggaagcttg
                                                                     60
cgttatccag gaagttggtg ttgaagaaac cccgctgatg aac
                                                                    103
<210> 10
<211> 106
<212> DNA
<213> chemical synthesis
<220>
<221> Unsure
<222> (1)..(106)
<400> 10
gaagaaaccc cgctgatgaa cgttgactcc atcctggctg ttaaaaaata cttccagcgt
                                                                     60
atcaccctgt acctgaccga aaaaaaatac tccccgtgcg cttggg
                                                                    106
<210> 11
<211> 112
<212> DNA
<213> chemical systhesis
<220>
<221> Unsure
<222> (1)..(112)
<400> 11
ttattcttta cgacgcagac gttcctgcag gttggtggac agggagaagg aacgcatgat
                                                                     60
ttcagcacga acaacttccc aagcgcacgg ggagtatttt ttttcggtca gg
                                                                    112
<210> 12
<211> 31
<212> DNA
```

<213> chemical synthesis